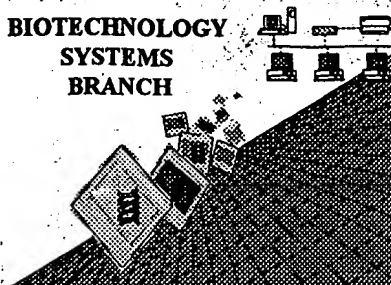# RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY SYSTEMS BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: ___09/772,134A___

Source: ___01PE___

Date Processed by STIC: ___12/18/01___

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
 PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
 PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by the treatment given to all mail coming via the Brentwood Mail Facility.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:
1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
    1911 South Clark Street, Crystal Mall One, Sequence Information, Arlington, VA 22202
           Or
   U.S. Patent and Trademark Office, 2011 South Clark Place, Customer Window, Box Sequence, Crystal Plaza Two,
    Lobby, Room 1B03, Arlington, Virginia 22202
4. Federal Express Delivery, 2011 South Clark Street, Crystal Plaza 2, Room 1B03-Mailroom, Box Sequence,
   Arlington, VA 22202

Raw Sequence Listing Error Summary .

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: <u>09 |772, 134A</u>

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
        Wrapped Aminos ·   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
                           prevent "wrapping."

2 _____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
        Numbering   use space characters, instead.

4 _____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
                    ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
                          each n or Xaa can only represent a single residue. Please present the maximum number of each
                          residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
        "bug"   sequences(s) _____ . Normally, PatentIn would automatically generate this section from the
                       previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
                       the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
                       Artificial or Unknown sequences.

7 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
        (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                            (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
                            (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
                            This sequence is intentionally skipped

                            Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
        (NEW RULES)   <210> sequence id number
                            <400> sequence id number
                            000

9 _√_ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
        (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
                            In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
         Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
                         is Artificial Sequence

11 _____ Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
                        Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
                        "Unknown." Please explain source of genetic material in <220> to <223> section.
                        (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
         "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
                        listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

**Does Not Comply
Corrected Diskette Needed**

Errors on pp. 3+4

```
   3 <110> APPLICANT: Lightfoot, David
   4        Meksem, Khalid
   6 <120> TITLE OF INVENTION: ISOLATED POLYNUCLEOTIDES AND POLYPEPTIDES RELATING TO LOCI
   7        UNDERLYING RESISTANCE TO SOYBEAN CYST NEMATODE AND SOYBEAN
   8        SUDDEN DEATH SYNDROME AND METHODS EMPLOYING SAME
  10 <130> FILE REFERENCE: 1268/4/2
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/772,134A
C--> 12 <141> CURRENT FILING DATE: 2001-12-18
  12 <150> PRIOR APPLICATION NUMBER: 60/178,811
  13 <151> PRIOR FILING DATE: 2000-01-28
  15 <160> NUMBER OF SEQ ID NOS: 122
  17 <170> SOFTWARE: PatentIn version 3.0
  19 <210> SEQ ID NO: 1
  20 <211> LENGTH: 87
  21 <212> TYPE: DNA
  22 <213> ORGANISM: soybean
  24 <400> SEQUENCE: 1
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  27 tgggtttctg ataaccgtgg tcgttaa                                             87
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  31 <211> LENGTH: 92
  32 <212> TYPE: DNA
  33 <213> ORGANISM: soybean
  35 <400> SEQUENCE: 2
  36 gaattcatgg tttctcttat cttatgacat tgttgccaag taatactact atataaattc        60
  38 agatttgggt ttcagataac cgtggtcgtt aa                                       92
  41 <210> SEQ ID NO: 3
  42 <211> LENGTH: 113
  43 <212> TYPE: DNA
  44 <213> ORGANISM: soybean
  46 <400> SEQUENCE: 3
  47 gaattcctaa tatacgagtg aatattattg taatgcttgt aaaaaaacat gataaaatgc        60
  49 aaaaatttgg ggtgaatttt tacgacatta gtgaaaaaaa catatccctt taa              113
  52 <210> SEQ ID NO: 4
  53 <211> LENGTH: 135
  54 <212> TYPE: DNA
  55 <213> ORGANISM: soybean
  57 <400> SEQUENCE: 4
  58 ttaaagggat atgttttttt cactaatgct gtaaaaattc acccagattt ttgcattttc        60
  60 tttgaaaaaa tgtactagat atatcatgtt tttttacaag cattacaata atattcactc       120
  62 gtatattagg aattc                                                        135
  65 <210> SEQ ID NO: 5
  66 <211> LENGTH: 116
  67 <212> TYPE: DNA
  68 <213> ORGANISM: soybean
  70 <400> SEQUENCE: 5
  71 gaattccggt tatctcagac aacttttgtt tggtttggtt atagtaaaga cacgattatc        60
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2nd ↓

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

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 73 caggctttga gaggcataga aataattttt ttatataaaa aaaaaagtct ctttaa        116
 76 <210> SEQ ID NO: 6
 77 <211> LENGTH: 113
 78 <212> TYPE: DNA
 79 <213> ORGANISM: soybean
 81 <400> SEQUENCE: 6
 82 gaatttcggt tatctcagac aacttttgtt tggtttggtt atagtaaaga cacgattatc     60
 84 caggctttga gaggcataga aataattttt ttatataaaa aaaagtctct tta           113
 87 <210> SEQ ID NO: 7
 88 <211> LENGTH: 409
 89 <212> TYPE: DNA
 90 <213> ORGANISM: soybean - Forrest
 92 <400> SEQUENCE: 7
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 95 gcaaacgata atataattat aagaaaaaga cacactttga gggcattttt gacttgagag    120
 97 aactcaggta tcaatctaaa agcaacgctg ttcaccttga gctgaaacac ctggaggaga    180
 99 aagcaaagca aaccaaacgc gagagagaaa taaagaacgg aaacagagag agagaggga    240
101 aggaccttgt tcaaagcaac ggggacaact ttagagccct ggcgcgcgtg ggggtcaata    300
103 agcgtaacct ggctgaggag agcctcggcg tcgtccttgc tgaagcagaa gaggaagagc    360
105 acgagaccaa gagaaactcc tcggaagcaa cgggaattgg tacgcagtc               409
108 <210> SEQ ID NO: 8
109 <211> LENGTH: 417
110 <212> TYPE: DNA
111 <213> ORGANISM: soybean
113 <400> SEQUENCE: 8
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116 actaaaatat ttgcaaacga taatataatt ataagaaaaa gactcacttt gagggcattt    120
118 ttgacttgag agaactcagg tatcaatcta aaagcaacgc tgttcacctt gagctgaaac    180
120 acctggagga gaaagcaaag caaaccaaac gcgagagaga aataaagaac ggaaacagag    240
122 agagaggaag gaccttgttc aaagcaacgg ggacaacttt agagccctgg cgcgcgtggg    300
124 ggtcaataag cgtaacctgg ctgaggagag cctcggcgcc gtccttgctg aagcagaaga    360
126 ggaagagccc gagaccaaga gaaactcctc ggaagcaacg ggaattggta cgcagtc       417
129 <210> SEQ ID NO: 9
130 <211> LENGTH: 165
131 <212> TYPE: DNA
132 <213> ORGANISM: soybean
134 <400> SEQUENCE: 9
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137 actttttttt attgaaaaaa tcgacccaag ttgaaacaca tgtttgagaa ttgttttgtg    120
139 catccaacgt ttttcttgta caatcagctg tgagagggga attgg                   165
142 <210> SEQ ID NO: 10
143 <211> LENGTH: 164
144 <212> TYPE: DNA
145 <213> ORGANISM: soybean
147 <400> SEQUENCE: 10
148 gagtaaatga aaatcgatca aaatcaaata atatatgctt tttttagttg ggttcaagta     60
150 cttttttttta ttgaaaaaat cgacccaagt tgaaacacat gtttgagaat tgttttgtgc    120
152 atccaacgtt tttcttgtac aatcagctgt gagaggggaa ttgg                     164
155 <210> SEQ ID NO: 11
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RAW SEQUENCE LISTING   DATE: 12/18/2001
PATENT APPLICATION: US/09/772,134A   TIME: 10:27:06

Input Set : **A:\seq list 1268-4-2.ST25.txt**
Output Set: **N:\CRF3\12182001\I772134A.raw**

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156 <211> LENGTH: 114
157 <212> TYPE: DNA
158 <213> ORGANISM: soybean
160 <400> SEQUENCE: 11
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163 ggaactgcta ttcttacttc taaatttttt attgacatcc aaagtgtgct ttaa          114
166 <210> SEQ ID NO: 12
167 <211> LENGTH: 114
168 <212> TYPE: DNA
169 <213> ORGANISM: soybean
171 <400> SEQUENCE: 12
172 gaattcccag ccagatttgt atcaaacatg tattgtccac aaaatgttca agcatcttag      60
174 ggaactgcta ttcttacttc taaatttttt attgacatcc aaagtgtgct ttaa          114
177 <210> SEQ ID NO: 13
178 <211> LENGTH: 3106
179 <212> TYPE: DNA
180 <213> ORGANISM: soybean
182 <220> FEATURE:
183 <221> NAME/KEY: misc_feature
184 <223> OTHER INFORMATION: n is an undetermined nucleotide (dATP, dCTP, dGTP, or dTTP)
187 <400> SEQUENCE: 13
188 aatgggagga gtgggaaaga cagtggctat ggagcttgtt ccggaggttg ggttggaatc      60
190 aagtgtgctc agggacaggt tattgtgatc cagcttcctt ggaagggttt gaggggtcga     120
192 atcaccgaca aaattggcca acttcaaggc ctcaggaagc ttagtcttca tgataaccaa     180
194 attggtggtt caatcccttc aactttggga cttcttccca accttagagg ggttcagtta     240
196 ttcaacaata ggcttacagg ttccatacct ctttctttag gtttctgcct ttgcttcaag     300
198 tctcttgacc tcagcaacaa cttgctcaca ggagcaatcc cttatagtct tgctaattcc     360
200 actaagcttt attggcttaa cttgagtttc aactccttct ctggtccttt accagctagc     420
202 ctaactcact catttctct cactttctt tctcttcaaa ataacaatct ttctggctcc     480
204 cttcctaact cttggggtgg gaattccaag aatggcttct ttaggcttca aaatttgatc     540
206 ctagatcata actttttcac tggtgacgtt cctgcttctt tgggtagctt aagagagctc     600
208 aatgagattt cccttagtca taataagttt agtggagcta taccaaatga aataggaacc     660
210 ctttctaggc ttaagacact tgacatttct aataatgcct tgaatgggaa cttgcctgct     720
212 accctctcta atttatcctc acttacactg ctgaatgcag agaacaacct ccttgacaat     780
214 caaatccctc aaagtttagg tagattgcgt aatctttctg ttctgatttt gagtagaaac     840
216 caatttagtg gacatattcc ttcaagcatt gcaaacattt cctcgcttag gcagcttgat     900
218 ttgtcactga ataatttcag tggagaaatt ccagtctcct ttgacagtca gcgcagtcta     960
220 aatctcttca atgtttccta caatagcctc tcaggttctg tcccccctct gcttgccaag    1020
222 aaatttaact caagctcatt tgtgggaaat attcaactat gtgggtacag cccttcaacc    1080
224 ccatgtcttt cccaagctcc atcacaagga gtcattgccc cacctcctga agtgtcaaaa    1140
226 catcaccatc ataggaagct aagcaccaaa gacataattc tcatagtagc aggagttctc    1200
228 ctcgtagtcc tgattatact ttgttgtgtc ctgctttct gcctgatcag aaagagatca    1260
230 acatctaggc cgggaacggc caagccaccc gagggtagag cggccactat gaggacagaa    1320
232 aaaggagtcc ctccagttgc tggtggtgat gttgaagcag gtggggaggc tggagggaaa    1380
234 ctagtccatt ttgatggacc aatggctttt acagctgatg atctcttgtg tgcaacagct    1440
236 gagatcatgg gaaagagcac ctatggaact gtttataagg ctattttgga ggatggaagt    1500
238 caagttgcag taaagagatt gagggaaaag atcactaaag gtcatagaga atttgaatca    1560
240 gaagtcagtg ttctaggaaa aattagacac cccaatgttt tggctctgag ggcctattac    1620
242 ttgggaccca aaggggaaaa gcttctgggt tttgatacat gtctaaagga agtcttgctt    1680
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RAW SEQUENCE LISTING   DATE: 12/18/2001
PATENT APPLICATION: US/09/772,134A   TIME: 10:27:06

Input Set : A:\seq list 1268-4-2.ST25.txt
Output Set: N:\CRF3\12182001\I772134A.raw

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      244 ctttcctaca tggaaggttc gtgtgctggt tctttcatta aagtgttgtg tgtgctggtc   1740
      246 tttaattata atttggagtt ttaccttagt aatctgtata attctaatcg gagaacagta   1800
W--> 248 caaacaaaaa cacctaagga acaacacctt anctttaata taccatatca ataaagtgaa   1860
      250 atattttctt ggtcatcttg atgcagggggg aactgaacat tcattattgg ccacaagatt   1920
      252 aaaatagccc aagccttggc ccgggcttgt ttgccttcat tcccaggaga acatcataca   1980
W--> 254 tgggacctcn catccagcaa tgtgtggctt gatgaaaaac aaatgctaaa attcagattt   2040
      256 tggtcttttt cgggttgatg tcaactgctg ctaattccaa cgtgatagct acagctggag   2100
      258 cattggatac cgggcacctg agctctcaaa gctcaagaaa gcaaacacta aaactgatat   2160
      260 ctacagtctt ggtgttatct tgttagaact cctaacgagg aaatcacctg gggtgtctat   2220
      262 gaatggacta gatttgcctc agtgggttgc ctcagttgtc aaagaggagt ggacaaatga   2280
      264 ggttttgat gcagacttga tgagagatgc atccacagtt ggcgacgagt tgctaaacac   2340
      266 gttgaagctc gctttgcact gtgttgatcc ttctccatca gcacgaccag aagttcatca   2400
      268 agttctccag cagctgaaga gattagacca gagagatcag tcacagccag tcccggggac   2460
      270 gatatcgtat agcacaaatt ttgcattgat ttttttgtgc caaatgtagt aggcctacta   2520
      272 tatatatgtt ctatgattct ttcattctta tattattttt gcctgtttga atgcttgaat   2580
      274 ttgtacatac tcatactaca ataaggtgta gttctggtta attttacctc tacctcaaag   2640
      276 ctggggtgta attctgtttc ctccaaggca cataatagtt gaaaatagtt ctcaggagca   2700
      278 ttcattgttt attctgcaag attctctttc acggctgcta tcttctatgc atgccctgcc   2760
      280 cataaatgca ttatgaagaa ttgtaacggc tgtgtttttg gacttcttca aaaagtttat   2820
      282 gttattgcca ggtgtatata tcaacatgtt ttaaagattt tcaaacaatc aggttttaga   2880
      284 tgtgggtttg catgcatgag attggactag tgcgcttgat gtagtataaa atataaattg   2940
      286 tccaatcaag caccctctac atgtccaaat aatgggcctt atgaaactta attttttaat   3000
W--> 288 tacaaactac agtaatcttt ttgaataaag atttacaaat tacaacngac atgtgaagcn   3060
W--> 290 gcatctttna ttgncaatct ttcaagttac tctattattt tctgcn              3106
      293 <210> SEQ ID NO: 14
      294 <211> LENGTH: 830
      295 <212> TYPE: PRT
      296 <213> ORGANISM: soybean
      298 <220> FEATURE:
      299 <221> NAME/KEY: misc_feature
      300 <223> OTHER INFORMATION: X is any amino acid
      303 <400> SEQUENCE: 14
      305 Asn Gly Arg Ser Gly Lys Asp Ser Gly Tyr Gly Ala Cys Ser Gly Gly
      306 1               5                   10                  15
      308 Trp Val Gly Ile Lys Cys Ala Gln Gly Gln Val Ile Val Ile Gln Leu
      309             20                  25                  30
      311 Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly Gln Leu
      312         35                  40                  45
      314 Gln Gly Leu Arg Lys Leu Ser Leu His Asp Asn Gln Ile Gly Gly Ser
      315     50                  55                  60
      317 Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val Gln Leu
      318 65                  70                  75                  80
      320 Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly Phe Cys
      321             85                  90                  95
      323 Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr Gly Ala
      324         100                 105                 110
      326 Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu Asn Leu
      327         115                 120                 125
      329 Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser Leu Thr His Ser
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[handwritten annotation:] → must give location of Xaa in ¿¿227, see error summary sheet, Item 9

RAW SEQUENCE LISTING   DATE: 12/18/2001
PATENT APPLICATION: US/09/772,134A   TIME: 10:27:06

Input Set : A:\seq list 1268-4-2.ST25.txt
Output Set: N:\CRF3\12182001\I772134A.raw

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330      130              .  135                140
332 Phe Ser Leu Thr Phe Leu Ser Leu Gln Asn Asn Asn Leu Ser Gly Ser
333 145              150              155              160
335 Leu Pro Asn Ser Trp Gly Gly Asn Ser Lys Asn Gly Phe Phe Arg Leu
336              165              170              175
338 Gln Asn Leu Ile Leu Asp His Asn Phe Phe Thr Gly Asp Val Pro Ala
339              180              185              190
341 Ser Leu Gly Ser Leu Arg Glu Leu Asn Glu Ile Ser Leu Ser His Asn
342          195              200              205
344 Lys Phe Ser Gly Ala Ile Pro Asn Glu Ile Gly Thr Leu Ser Arg Leu
345      210              215              220
347 Lys Thr Leu Asp Ile Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro Ala
348 225              230              235              240
350 Thr Leu Ser Asn Leu Ser Ser Leu Thr Leu Leu Asn Ala Glu Asn Asn
351              245              250              255
353 Leu Leu Asp Asn Gln Ile Pro Gln Ser Leu Gly Arg Leu Arg Asn Leu
354          260              265              270
356 Ser Val Leu Ile Leu Ser Arg Asn Gln Phe Ser Gly His Ile Pro Ser
357          275              280              285
359 Ser Ile Ala Asn Ile Ser Ser Leu Arg Gln Leu Asp Leu Ser Leu Asn
360      290              295              300
362 Asn Phe Ser Gly Glu Ile Pro Val Ser Phe Asp Ser Gln Arg Ser Leu
363 305              310              315              320
365 Asn Leu Ser Asn Val Ser Tyr Asn Ser Leu Ser Gly Ser Val Pro Pro
366          325              330              335
368 Leu Leu Ala Lys Lys Phe Asn Ser Ser Ser Phe Val Gly Asn Ile Gln
369          340              345              350
371 Leu Cys Gly Tyr Ser Pro Ser Thr Pro Cys Leu Ser Gln Ala Pro Ser
372          355              360              365
374 Gln Gly Val Ile Ala Pro Pro Pro Glu Val Ser Lys His His His His
375      370              375              380
377 Arg Lys Leu Ser Thr Lys Asp Ile Ile Leu Ile Val Ala Gly Val Leu
378 385              390              395              400
380 Leu Val Val Leu Ile Ile Leu Cys Cys Val Leu Leu Phe Cys Leu Ile
381          405              410              415
383 Arg Lys Arg Ser Thr Ser Lys Ala Gly Asn Gly Gln Ala Thr Glu Gly
384          420              425              430
386 Arg Ala Ala Thr Met Arg Thr Glu Lys Gly Val Pro Pro Val Ala Gly
387          435              440              445
389 Gly Asp Val Glu Ala Gly Gly Glu Ala Gly Gly Lys Leu Val His Phe
390      450              455              460
392 Asp Gly Pro Met Ala Phe Thr Ala Asp Asp Leu Leu Cys Ala Thr Ala
393 465              470              475              480
395 Glu Ile Met Gly Lys Ser Thr Tyr Gly Thr Val Tyr Lys Ala Ile Leu
396          485              490              495
398 Glu Asp Gly Ser Gln Val Ala Val Lys Arg Leu Arg Glu Lys Ile Thr
399          500              505              510
401 Lys Gly His Arg Glu Phe Glu Ser Glu Val Ser Val Leu Gly Lys Ile
402          515              520              525
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VERIFICATION SUMMARY   DATE: 12/18/2001
PATENT APPLICATION: **US/09/772,134A**   TIME: 10:27:07

Input Set : **A:\seq list 1268-4-2.ST25.txt**
Output Set: **N:\CRF3\12182001\I772134A.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:248 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:248 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:254 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:288 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:290 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:419 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:422 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:422 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
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L:425 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:428 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:428 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:434 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:434 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:437 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:437 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:446 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:452 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:455 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:467 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:475 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
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L:497 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:506 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
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L:563 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:574 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18

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           VERIFICATION SUMMARY              DATE: 12/18/2001
           PATENT APPLICATION:  US/09/772,134A     TIME: 10:27:07

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L:615 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
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L:639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
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L:645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:683 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:683 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:685 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
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L:687 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
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L:689 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:717 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:717 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:719 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:719 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
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L:721 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:723 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:723 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:725 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:725 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:727 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
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VERIFICATION SUMMARY   DATE: 12/18/2001
PATENT APPLICATION: US/09/772,134A   TIME: 10:27:07

Input Set : **A:\seq list 1268-4-2.ST25.txt**
Output Set: **N:\CRF3\12182001\I772134A.raw**

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L:945 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27
L:961 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
L:963 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28
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CProject   ~~

CProjectData   ŶISOLATED POLYNUCLEOTIDES AND POLYPEPTIDES RELATING
TO LOCI UNDERLYING RESISTANCE TO SOYBEAN CYST NEMATODE AND SOYBEAN
SUDDEN DEATH SYNDROME AND METHODS EMPLOYING SAME 1268/4/2
_____-___-__   z   ~~

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   DNA   ?
                   ¤   ?   E-CTA/ M-AGG113
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120
gtatattagg aattc
135   agctrymkswbdhvn   DNA   ?
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Appendix A To Subpart G to Part 1—Sample Sequence Listing

<110> Smith, John

Smith, Jane

<120> Example of a Sequence Listing

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<302> Isolation and Characterization of a Gene Encoding a

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<303> Journal of Fictional Genes
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ctttcgcggc agcggcggcg ctttccggcg cgcgcccgtc cgcccctaga cctgagaggt   300

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<211> 18

<212> PRT

<213> Paramecium aurelia

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